



Figure S2. Neighbour Joining phylogenetic tree obtained from the SNPs in the portion of the multiple alignment shared by all strains. The alignment includes 64 strains of *N. meningitidis*, *N. gonorrhoeae*, *N. polysaccharea* and *N. lactamica* of which 6 have a duplicated sequence retrieved from multiple genome sequencing projects. The (\$) symbol indicates sequences that were downloaded from the BigsDB database, otherwise from GenBank. The presence of *fHbp*, *nhba* and *nadA* is indicated. For *fHbp* the colours indicate the major allelic variants, asterisks (*) indicate genes that were frameshifted, at the border of a contig or interrupted by the an IS.